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<!--StartFragment-->RESULT 7
US-09-938-842A-1120
; Sequence 1120, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
;  APPLICANT: Harper, Jeff
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;  TITLE OF INVENTION:  SAME, AND METHODS OF USE
;  FILE REFERENCE: SCRIP1300-3
;  CURRENT APPLICATION NUMBER: US/09/938,842A
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/227,866
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1120
;   LENGTH: 1977
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-1120

Alignment Scores:
Pred. No.:              1.12e-182      Length:         1977
Score:                  1909.00        Matches:        356
Percent Similarity:     74.8%          Conservative:   115
Best Local Similarity:  56.5%          Mismatches:     117
Query Match:            53.7%          Indels:         42
DB:                     3              Gaps:           7

US-10-544-180A-2 (1-673) x US-09-938-842A-1120 (1-1977)

Qy        75 LeuPheSerLysGluIleLeuAspValIleAlaThrSerThrAlaAspLeuGlyProLeu 94
             |||  ||::::::::::  :::::::::::|||||   :::        :::     :::
Db       118 CTGTTATCTCAGGATGTG---AACATAGTTGCGACATACAGTGACCATTACGGCAATATA 174

Qy        95 SerLeuAspSerPheLysLysAsnAsnLeuSerAlaSerTrpArgGlyThrGlyValAsp 114
             |||        |||    :::|||||| |||||||
Db       175 CGCCTTGGTAGGGTGAAAATGGGGGATCTTTCACCTTCTTGG------------------ 216

Qy       115 ProSerPheArgHisSerGluAsnProAla---------ThrProAspValLysSerAsn 131
             ||||||||||||        :::        |||   :::
Db       217 ------------GTTTTGGAGAATCCTGCCTATCAAGTTAGCCGCAAAACAAAAGGTTCG 264

Qy       132 AsnLeuAsnGluLysArgAspSerIleSerLysAsp----------------------- 143
             |||    ||||||||||        |||
Db       265 CAGCTAGTTATACCACGGGATTCATTTCAAATGATACTGGAATGGAAGATAATGCAAGC 324

Qy       144 ------SerIleHisGlnLysValGlu--------------------------------- 150
               :::   :::|||       |||
Db       325 CATTCTACAACTAATCAGACTGATGAAAGCGAAAATCAGTTTCCAAACGTGGATTTTGCA 384

Qy       151 ThrProThrLysIleHisArgArgGlnLeuArgGluLysArgGluMetArgAlaAsn 170
             :::|||   |||::::   |||::::   ||||||:::::::||||||        |||
Db       385 AGCCCAGCAAAACTGAAGCGGCAGATTTTACGTCAGGAAAGGAGAGGTCAACGAACTTTA 444
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Qy     171 GluLeuValGlnHisAsnAspAspThrIleLeuLysLeuGluAsnAlaAlaIleGluArg 190
           ||||||:::::        :::|||       :::::::::   ||||||||||:::::
Db     445 GAGCTGATCCGACAGAAAAGGAAACTGATGAGCAGATGCAAGAAGCAGCCATTCAGAAG 504

Qy     191 SerLysSerValAspSerAlaValLeuGlyLysTyrSerIleTrpArgArgGluAsnGlu 210
           |||   |||  :::::::::::||::||||||||||||||||||||:::   |||
Db     505 TCAATGAGCTTTGAAAACTCAGTCATAGGGAAATACAGTATATGGAGGAGAGACTATGAG 564

Qy     211 AsnAspAsnSerAspSerAsnIleArgLeuMetArgAspGlnValIleMetAlaArgVal 230
           :::   |||::|||:::  :::::||||||||||||:::||||||||||||||:::::::
Db     565 AGCCCAAATGCTGATGCTATCTTGAAGCTTATGAGAGACCAGATCATAATGGCAAAAGCA 624

Qy     231 TyrSerGlyIleAlaLysLeuLysAsnLysAsnAspLeuLeuGlnGluLeuGlnAlaArg 250
           ||:::   |||||||||  ||||||   :::|||        |||       :::
Db     625 TATGCAAATATTGCCAAATCAAAAAATGTAACCAATCTGTACGTTTCTTGATGCAGCAG 684

Qy     251 LeuLysAspSerGlnArgValLeuGlyGluAlaThrSerAspAlaAspLeuProArgSer 270
           :::::::::||||||::|||:::||||||||||||||||||||||||||   |||
Db     685 TGTGGAGAAAATAAACGTGTTATAGGTAAAGCAACCTCTGATGCTGACCTTCCTTCAAGC 744

Qy     271 AlaHisGluLysLeuArgAlaMetGlyValGlnValLeuAlaLysAlaLysMetGlnLeuTyr 290
           |||  :::::  :::|||||||||      |||::  ||||||  ||||||  :::
Db     745 GCTCTTGATCAAGCAAAAGCCATGGGCCATGCACTCTCTCTTGCAAAAGACGAGTTATAT 804

Qy     291 AspCysLysLeuValThrGlyLysLeuArgAlaMetLeuGlnThrAlaAspGluGlnVal 310
           ||||||   :::   |||   |||||||:::|||||||||   :::   :::|||
Db     805 GACTGCCATGAACTTGCAAAAAAGTTCCGGGCCATCCTTCAGTCCACTGAACGCCAAGTA 864

Qy     311 ArgSerLeuLysLysGlnSerThrPheLeuAlaGlnLeuAlaAlaLysThrIleProAsn 330
           |||||||||:::   |||||||||      |||||||||||||||||||||||
Db     865 GATGGACTGAAGAAAAAGGGAACCTTCTTAATTCAGCTAGCTGCCAAACATTTCCCAAG 924

Qy     331 ProIleHisCysLeuSerMetArgLeuThrIleAspTyrTyrLeuLeuSerProGluLys 350
           |||::||||||||||||||:::::|||   |||||||||:|||||||||   :::
Db     925 CCATTGCATTGCCTGAGTCTGCAGCTAGCGGCAGACTATTTTATTCTAGGTTTCAATGAA 984

Qy     351 ArgLysPheProArgSerGlu------------AsnLeuGluAsnProAsnLeuTyrHis 366
           :::   :::           |||||||:::|||:::|||||||||
Db     985 GAGGATGCAGTGAAAGAGGATGTCAGTCAAAAGAAGCTTGAAGATCCTTCGCTCTATCAC 1044

Qy     367 TyrAlaLeuPheSerAspAsnValLeuAlaAlaSerValValValAsnSerThrIleMet 386
           |||||||:::|||||||||||||||||||  |||||||||||||||||||||:::::::
Db    1045 TATGCGATCTTTTCGGATAACGTTCTGGCTACATCAGTGGTGGTGAACTCCACTGTCTTG 1104

Qy     387 AsnAlaLysAspProSerLysHisValPheHisLeuValThrAspLysLeuAsnPheGly 406
           |||||||||::||||   :::|||||||||||:::||||||||||||||||||||||
Db    1105 AATGCAAAGGAACCGCAGAGGCATGTGTTCCATATAGTAACTGACAAACTGAATTTTGGT 1164

Qy     407 AlaMetAsnMetTrpPheLeuLeuAsnProProGlyLysAlaThrIleHisValGluAsn 426
           |||||||   |||||||||   ::|||   |||       |||||||||   |||||||||
Db    1165 GCAATGAAGATGTGGTTTCGCATCAATGCTCCTGCTGATGCGACGATTCAAGTTGAAAAC 1224

Qy     427 ValAspGluPheLysTrpLeuAsnSerSerTyrCysProValLeuArgGlnLeuGluSer 446
           :::::::::|||||||||||||||||||   :::   ||||||||||||||||||||
Db    1225 ATAAATGATTTCAAGTGGCTGAACTCCTCTTACTGCTCTGTTCTACGGCAGCTTGAATCT 1284

Qy     447 AlaAlaMetArgGluTyrTyrPheLysAlaAspHisProThrSer---------GlySer 463
           |||   :::::||||||||||||||:::::::::::||||||:::   ||:::
Db    1285 GCAAGGCTGAAAGAATACTATTTCAAAGCAAATCATCCTTCATCAATCTCAGCTGGCGCA 1344

Qy     464 SerAsnLeuLysTyrArgAsnProLysTyrLeuSerMetLeuAsnHisLeuArgPheTyr 483
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             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1345 GATAATCTAAAGTACCGCAACCCAAAGTATCTATCGATGCTGAATCATCTCAGATTCTAC 1404

Qy    484 LeuProGluValTyrProLysLeuAsnLysIleLeuPheLeuAspAspAspIleIleVal 503
             |||||||||||||||||||||||    |||||||||||||||||||||||||:::|||
Db   1405 CTTCCTGAGGTTTATCCGAGCTGGAGAAGATTCTGTTTCTAGACGATGACATTGTGGTG 1464

Qy    504 GlnLysAspLeuThrProLeuTrpGluValAsnLeuAsnGlyLysValAsnGlyAlaVal 523
             |||||||||    |||||||||:::::::::    |||||||||||||||||||||
Db   1465 CAGAAGGACCTGGCACCACTATGGGAAATAGACATGCAAGGAAAAGTGAATGGTGCGGTG 1524

Qy    524 GluThrCysGlyGluSerPheHisArgPheAspLysTyrLeuAsnPheSerAsnProHis 543
             |||||||||    |||||||||||||||||||||||||||||||||||||||||||
Db   1525 GAGACGTGCAAGGAGAGCTTCCACAGATTTGACAAGTACCTCAACTTCTCAAATCCAAAG 1584

Qy    544 IleAlaArgAsnPheAsnProAsnAlaCysGlyTrpAlaTyrGlyMetAsnMetPheAsp 563
             |||::    |||||:::    ||||||||||||||||||||||||||||||||||
Db   1585 ATTTCAGAGAATTTTGACGCTGGTGCTTGTGGGTGGGCATTTGGGATGAATATGTTTGAC 1644

Qy    564 LeuLysGluTrpLysLysArgAspIleThrGlyIleTyrHisLysTrpGlnAsnMetAsn 583
             ||||||||||:::|||||:::|||||||||||||||||||||||||:::::::|||
Db   1645 CTGAAAGAGTGGAAGAAACGGAACATTACAGGGATATATCACTATTGGCAAGACTTGAAT 1704

Qy    584 GluAsnArgThrLeuTrpLysLeuGlyThrLeuProProGlyLeuIleThrPheTyrGly 603
             |||:::||||||||||||||||||||:::|||||||||||||||||||||||||||
Db   1705 GAAGACAGAACACTGTGGAAGCTGGGATCGTTGCCACCGGGGCTGATAACATTTTACAAC 1764

Qy    604 LeuThrHisProLeuAsnLysAlaTrpHisValLeuGlyLeuGlyTyrAsnProSerIle 623
             ||||||:::    :::::::::::|||||||||||||||||||||:::||:::::::
Db   1765 CTGACGTATGCAATGGATAGGAGCTGGCACGTACTAGGGCTGGGATATGACCCAGCGCTA 1824

Qy    624 AspLysLysAspIleGluAsnAlaAlaValValHisTyrArgAsnGlyAsnMetLysProTrp 643
             ::::::    |||||||||||||||||||||||||||||||    ||||||||||
Db   1825 AACCAAACAGCAATAGAGAATGCAGCGGTAGTGCATTACAATGGGAACTACAAGCCATGG 1884

Qy    644 LeuGluLeuAlaMetSerLysTyrArgProTyrTrpThrLysTyrIleLysPheAspHis 663
             |||   ||||||    :::|||||:::||||||:::|||::::::::|||::::
Db   1885 CTGGGTTTAGCATTCGCCAAGTACAAACCGTACTGGTCCAAGTACGTTGAGTACGACAAC 1944

Qy    664 ProTyrLeuArgArgCysAsnLeuHisGlu 673
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Db   1945 CCTTATCTCCGACGGTGCGACATCAATGAA 1974

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